



1

SEQUENCE LISTING

<110> HUGANIR, RICHARD L.
KIM, GJEEHAE

<120> SIGNAL TRANSDUCING SYNAPTIC MOLECULES AND USES THEREOF

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<140> 09/294,298

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<150> 60/082,690

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<170> PatentIn Ver. 2.1

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 1330 1335 1340
 Pro Ser Val Thr Asp Leu Leu Pro Ser Ala Pro Asp Pro Gly Thr Ser
 1345 1350 1355 1360
 Pro Thr Thr Arg Thr Gly Arg His Gln Gly Thr Ala Gly Leu Ser Pro
 1365 1370 1375
 Leu Thr Pro Pro Trp Gly Thr His Leu Ser Thr Pro Leu Leu His Ser
 1380 1385 1390
 Arg Arg Glu Ser Gly Thr Leu Ser Cys Pro Leu Thr Pro Gly His His
 1395 1400 1405
 Leu Pro His Thr Asp Pro Phe Thr Leu Gly Cys Tyr Pro His Pro
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<211> 4134

<212> DNA

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<220>

<223> Description of Unknown Organism: mammalian
SYNGAP-B

<220>

<221> CDS

<222> (4)..(3741)

<220>

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<222> (3745)..(4134)

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tgc ccc ctc ctt ccc acc gcc agc ctc tcc gcc gcc gct gct ctt cct	96
Cys Pro Leu Leu Pro Thr Ala Ser Leu Ser Ala Ala Ala Ala Leu Pro	
20 25 30	
gct gct ttc cgg ggg aat acc act tgg gtc gct cga gga gga aga gtg	144
Ala Ala Phe Arg Gly Asn Thr Thr Trp Val Ala Arg Gly Gly Arg Val	
35 40 45	
tcc ccg ggg ggg aaa cag tac agc atg gaa gcc gcc ccc gct gcg ccc	192
Ser Pro Gly Gly Lys Gln Tyr Ser Met Glu Ala Ala Pro Ala Ala Pro	
50 55 60	
ttc cgg ccc tcg caa ggc ttc ctg agc cgg agg cta aaa agc tcc atc	240
Phe Arg Pro Ser Gln Gly Phe Leu Ser Arg Arg Leu Lys Ser Ser Ile	
65 70 75	
aaa cgt aca aag tca caa ccc aaa ctt gac cgg acc agc agc ttt cga	288
Lys Arg Thr Lys Ser Gln Pro Lys Leu Asp Arg Thr Ser Ser Phe Arg	
80 85 90 95	
cag atc ctg cct cgc ttc cga agt gct gac cat gac cgg gcc cgg ctg	336
Gln Ile Leu Pro Arg Phe Arg Ser Ala Asp His Asp Arg Ala Arg Leu	
100 105 110	
atg cag agc ttc aag gag tct cac tcc cat gag tcc ctg ctg agt ccc	384
Met Gln Ser Phe Lys Glu Ser His Ser His Glu Ser Leu Leu Ser Pro	
115 120 125	
agc agt gct gct gag gcc ctg gag ctc aac ctg gat gaa gac tcc att	432
Ser Ser Ala Ala Glu Ala Leu Glu Leu Asn Leu Asp Glu Asp Ser Ile	
130 135 140	
atc aag cca gta cac agc tcc atc ctg ggc cag gag ttc tgc ttt gag	480
Ile Lys Pro Val His Ser Ser Ile Leu Gly Gln Glu Phe Cys Phe Glu	
145 150 155	

gta aca aca tcg tct ggg aca aaa tgt ttt gcc tgt cgg tct gca gcc Val Thr Thr Ser Ser Gly Thr Lys Cys Phe Ala Cys Arg Ser Ala Ala 160 165 170 175	528
gaa agg gac aaa tgg att gag aat cta cag agg gct gtg aaa ccc aac Glu Arg Asp Lys Trp Ile Glu Asn Leu Gln Arg Ala Val Lys Pro Asn 180 185 190	576
aag gac aac agc cgc cgg gta gat aac gtg ctg aaa cta tgg atc ata Lys Asp Asn Ser Arg Arg Val Asp Asn Val Leu Lys Leu Trp Ile Ile 195 200 205	624
gaa gct cga gag ctg ccc ccc aag aag cga tat tac tgc gag tta tgc Glu Ala Arg Glu Leu Pro Pro Lys Lys Arg Tyr Tyr Cys Glu Leu Cys 210 215 220	672
ctg gac gac atg ctc tat gca cgg acc act tcc aag ccc cgc tca gcc Leu Asp Asp Met Leu Tyr Ala Arg Thr Thr Ser Lys Pro Arg Ser Ala 225 230 235	720
tca gga gac act gtc ttt tgg ggc gag cac ttc gag ttt aac aac ctg Ser Gly Asp Thr Val Phe Trp Gly Glu His Phe Glu Phe Asn Asn Leu 240 245 250 255	768
cct gct gtc cgg gcg ctg cgg ctg cat ctg tac cgt gac tcg gac aaa Pro Ala Val Arg Ala Leu Arg Leu His Leu Tyr Arg Asp Ser Asp Lys 260 265 270	816
aag cgg aag aag gac aag gca ggc tac gtt ggc ctg gtg act gtt cca Lys Arg Lys Lys Asp Lys Ala Gly Tyr Val Gly Leu Val Thr Val Pro 275 280 285	864
gtg gcc acc ctg gct ggg cgc cac ttc aca gag cag tgg tac ccc gtg Val Ala Thr Leu Ala Gly Arg His Phe Thr Glu Gln Trp Tyr Pro Val 290 295 300	912
acc ctg cca aca gga agt ggg ggc tct ggg ggt atg ggc tcg ggg gga Thr Leu Pro Thr Gly Ser Gly Gly Ser Gly Gly Met Gly Ser Gly Gly 305 310 315	960
gga ggg ggg tca ggg ggc ggc tca ggg ggc aaa ggg aaa gga ggc tgt Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Lys Gly Lys Gly Gly Cys 320 325 330 335	1008
cct gct gtg cgg ctg aag gcc cgt tac cag aca atg agt atc ctg ccc Pro Ala Val Arg Leu Lys Ala Arg Tyr Gln Thr Met Ser Ile Leu Pro 340 345 350	1056
atg gag cta tat aag gag ttt gca gaa tat gtg acc aac cac tac cgc Met Glu Leu Tyr Lys Glu Phe Ala Glu Tyr Val Thr Asn His Tyr Arg 355 360 365	1104
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ata gaa gag tat atg aga ctg att ggc cag aaa tac ctc aag gat gcc Ile Glu Glu Tyr Met Arg Leu Ile Gly Gln Lys Tyr Leu Lys Asp Ala 435 440 445	1344
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gta gac ccc atc aag tgc aca gcg tcc agt ctg gca gag cac cag gcc Val Asp Pro Ile Lys Cys Thr Ala Ser Ser Leu Ala Glu His Gln Ala 465 470 475	1440
aac ctg cgg atg tgc tgt gag ttg gcc ctg tgc aag gtg gtc aac tcc Asn Leu Arg Met Cys Cys Glu Leu Ala Leu Cys Lys Val Val Asn Ser 480 485 490 495	1488
cat tgc gtg ttc ccg agg gag ctg aag gag gtg ttt gca tca tgg cgg His Cys Val Phe Pro Arg Glu Leu Lys Glu Val Phe Ala Ser Trp Arg 500 505 510	1536
ctg cgc tgt gca gag cgg ggc cgg gag gac att gct gac agg ctg atc Leu Arg Cys Ala Glu Arg Gly Arg Glu Asp Ile Ala Asp Arg Leu Ile 515 520 525	1584
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agt ctg ttt gga ctg atg cag gag tac cca gat gag cag acc tca cga Ser Leu Phe Gly Leu Met Gln Glu Tyr Pro Asp Glu Gln Thr Ser Arg 545 550 555	1680
acc ctc acc ctc atc gcc aag gtt atc cag aac ctg gcc aac ttt tcc Thr Leu Thr Leu Ile Ala Lys Val Ile Gln Asn Leu Ala Asn Phe Ser 560 565 570 575	1728
aag ttt acc tca aag gag gac ttc ctg ggc ttc atg aac gag ttt ctg Lys Phe Thr Ser Lys Glu Asp Phe Leu Gly Phe Met Asn Glu Phe Leu 580 585 590	1776
gag ctg gag tgg ggt tct atg cag caa ttc ttg tat gag ata tcc aac Glu Leu Glu Trp Gly Ser Met Gln Gln Phe Leu Tyr Glu Ile Ser Asn 595 600 605	1824

ctg gac aca ctg acc aac agc agc agt ttt gag ggc tac ata gac ttg Leu Asp Thr Leu Thr Asn Ser Ser Ser Phe Glu Gly Tyr Ile Asp Leu 610 615 620	1872
ggc cgc gag ctc tcc aca ctt cac gcc ctg ctc tgg gag gtg ctg ccc Gly Arg Glu Leu Ser Thr Leu His Ala Leu Leu Trp Glu Val Leu Pro 625 630 635	1920
cag ctc agc aag gaa gcc ctc ctg aag ctg ggc ccg ctg ccc cgg ctc Gln Leu Ser Lys Glu Ala Leu Leu Lys Leu Gly Pro Leu Pro Arg Leu 640 645 650 655	1968
ctc agc gac atc agc aca gcc ctg agg aac cct aac atc caa agg cag Leu Ser Asp Ile Ser Thr Ala Leu Arg Asn Pro Asn Ile Gln Arg Gln 660 665 670	2016
ccg agc cgc cag agc gag cgc gct cgg tct cag ccc atg gtg ctg cgc Pro Ser Arg Gln Ser Glu Arg Ala Arg Ser Gln Pro Met Val Leu Arg 675 680 685	2064
ggg ccg tca gcc gag atg cag ggc tac atg atg cgg gac ctc aac agc Gly Pro Ser Ala Glu Met Gln Gly Tyr Met Met Arg Asp Leu Asn Ser 690 695 700	2112
tcc atc gac ctt cag tcc ttc atg gct cga ggc ctc aac agc tct atg Ser Ile Asp Leu Gln Ser Phe Met Ala Arg Gly Leu Asn Ser Ser Met 705 710 715	2160
gac atg gct cgc ctc ccc tcc cca acc aag gag aaa ccc ccg ccg ccc Asp Met Ala Arg Leu Pro Ser Pro Thr Lys Glu Lys Pro Pro Pro 720 725 730 735	2208
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gcc cgg tcc tcc cca gca tac tgc acg agc agc tcg gac atc aca gag Ala Arg Ser Ser Pro Ala Tyr Cys Thr Ser Ser Ser Asp Ile Thr Glu 755 760 765	2304
ccg gag cag aag atg ctg agt gtc aac aag agt gtg tcc atg ctg gac Pro Glu Gln Lys Met Leu Ser Val Asn Lys Ser Val Ser Met Leu Asp 770 775 780	2352
ctg cag ggc gac ggg cct ggg ggc cgc ctt aac agc agt agt gtt tcc Leu Gln Gly Asp Gly Pro Gly Gly Arg Leu Asn Ser Ser Ser Val Ser 785 790 795	2400
aac ctg gca gct gtt ggg gac ctg ttg cac tca agc cag gct tca ctg Asn Leu Ala Ala Val Gly Asp Leu Leu His Ser Ser Gln Ala Ser Leu 800 805 810 815	2448
aca gca gcc ttg ggg ttg cgg cct gca cct gcc ggg cgc ctc tcc caa Thr Ala Ala Leu Gly Leu Arg Pro Ala Pro Ala Gly Arg Leu Ser Gln 820 825 830	2496

ggg agt ggc tct tcc atc aca gca gcc ggc atg cgc ctc agc cag atg Gly Ser Gly Ser Ser Ile Thr Ala Ala Gly Met Arg Leu Ser Gln Met 835 840 845	2544
ggg gtc act acg gat ggt gtc ccc gcc cag caa ctg cgc atc cct ctt Gly Val Thr Thr Asp Gly Val Pro Ala Gln Gln Leu Arg Ile Pro Leu 850 855 860	2592
tcc ttc cag aac cct ctc ttc cat atg gct gcc gat gga cca ggg ccc Ser Phe Gln Asn Pro Leu Phe His Met Ala Ala Asp Gly Pro Gly Pro 865 870 875	2640
cca gca ggc cat gga ggg agc agt ggc cat ggt cca cct tcc tcc cat Pro Ala Gly His Gly Gly Ser Ser Gly His Gly Pro Pro Ser Ser His 880 885 890 895	2688
cac cac cac cac cac cat cac cat cac cga ggg gga gaa ccc cca ggg His His His His His His His His His Arg Gly Gly Glu Pro Pro Gly 900 905 910	2736
gac act ttt gcc ccg ttc cat ggc tat agc aag agc gag gac ctc tct Asp Thr Phe Ala Pro Phe His Gly Tyr Ser Lys Ser Glu Asp Leu Ser 915 920 925	2784
aca ggg gtc cct aag ccc cct gcg gcc tcc atc ctt cac agc cac agc Thr Gly Val Pro Lys Pro Pro Ala Ala Ser Ile Leu His Ser His Ser 930 935 940	2832
tac agt gat gag ttt gga ccc tct ggt act gat ttt acc cgt cgg cag Tyr Ser Asp Glu Phe Gly Pro Ser Gly Thr Asp Phe Thr Arg Arg Gln 945 950 955	2880
ctc tca ctt cag gac aac cta cag cac atg ctc tcc ccg ccc cag atc Leu Ser Leu Gln Asp Asn Leu Gln His Met Leu Ser Pro Pro Gln Ile 960 965 970 975	2928
acc atc ggt ccc cag agg cca gct ccc tca ggg cca gga ggg ggc agt Thr Ile Gly Pro Gln Arg Pro Ala Pro Ser Gly Pro Gly Gly Gly Ser 980 985 990	2976
ggg ggg ggc agt ggt ggg ggc ggt ggg ggc cag cca cct ccc ttg cag Gly Gly Gly Ser Gly Gly Gly Gly Gly Gly Gln Pro Pro Pro Leu Gln 995 1000 1005	3024
agg ggc aaa tct cag cag ttg aca gtg agt gct gcc cag aaa ccc cgg Arg Gly Lys Ser Gln Gln Leu Thr Val Ser Ala Ala Gln Lys Pro Arg 1010 1015 1020	3072
ccg tcc agc ggg aac cta ttg cag tcc ccg gaa cca agt tat ggt cct Pro Ser Ser Gly Asn Leu Leu Gln Ser Pro Glu Pro Ser Tyr Gly Pro 1025 1030 1035	3120
gcc cgt cca cgg caa cag agc ctc agc aaa gag ggc agc att ggg ggc Ala Arg Pro Arg Gln Gln Ser Leu Ser Lys Glu Gly Ser Ile Gly Gly 1040 1045 1050 1055	3168

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gcc tcg gag cgg act gta gcc tgg gtg tcc aat atg cct cac ctg tcc Ala Ser Glu Arg Thr Val Ala Trp Val Ser Asn Met Pro His Leu Ser 1090 1095 1100	3312
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tac gag gag gag atc cac tca ctg aag gaa agg cta cac atg tcc aac Tyr Glu Glu Glu Ile His Ser Leu Lys Glu Arg Leu His Met Ser Asn 1140 1145 1150	3456
cgg aag ctg gaa gag tac gag cgg agg ctg ctg tcc cag gaa gag cag Arg Lys Leu Glu Glu Tyr Glu Arg Arg Leu Leu Ser Gln Glu Glu Gln 1155 1160 1165	3504
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atc att ggc agg ctg atg ctg gtg gag gag gag ctg cgc cgg gac cac Ile Ile Gly Arg Leu Met Leu Val Glu Glu Glu Leu Arg Arg Asp His 1200 1205 1210 1215	3648
ccc gcc atg gct gag ccg ctg cct gaa ccc aag aag agg ctg ctc gac Pro Ala Met Ala Glu Pro Leu Pro Glu Pro Lys Lys Arg Leu Leu Asp 1220 1225 1230	3696
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tga cgc tgg ccc cac ctt gga acg gcc tgg ccc ccc cag ccc cac ccc Arg Trp Pro His Leu Gly Thr Ala Trp Pro Pro Gln Pro His Pro 1250 1255 1260	3789
ccc cac ccc ggc tgc aga tca cag aga acg gcg agt tcc gga aca ccg Pro His Pro Gly Cys Arg Ser Gln Arg Thr Ala Ser Ser Gly Thr Pro 1265 1270 1275	3837

cag acc act agc cca ccc agc atc aca gac ctc ctt ccc tgt gca ccc 3885
 Gln Thr Thr Ser Pro Pro Ser Ile Thr Asp Leu Leu Pro Cys Ala Pro
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 Tyr Pro Gly Pro Pro Ser Val Thr Asp Leu Leu Pro Ser Ala Pro Asp
 1295 1300 1305
 cct gga aca tca cca acc acc agg act gga cgt cac caa ggg aca gcg 3981
 Pro Gly Thr Ser Pro Thr Thr Arg Thr Gly Arg His Gln Gly Thr Ala
 1310 1315 1320 1325
 gga ttg tct ccc tta acg cct cct tgg ggc acc cat ctg tca acc cca 4029
 Gly Leu Ser Pro Leu Thr Pro Pro Trp Gly Thr His Leu Ser Thr Pro
 1330 1335 1340
 ctg ctc cat tcc agg agg gag agt ggg acc ctc agc tgc cct ctc acc 4077
 Leu Leu His Ser Arg Arg Glu Ser Gly Thr Leu Ser Cys Pro Leu Thr
 1345 1350 1355
 cca gga cac cac cta ccc cac aca gac ccc ttc act ctg ggg tgc tat 4125
 Pro Gly His His Leu Pro His Thr Asp Pro Phe Thr Leu Gly Cys Tyr
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 Pro His Pro
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<210> 4

<211> 1376

<212> PRT

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<220>

 <223> Description of Unknown Organism: mammalian
 SYNGAP-B

<400> 4

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 20 25 30
 Ala Phe Arg Gly Asn Thr Thr Trp Val Ala Arg Gly Gly Arg Val Ser
 35 40 45
 Pro Gly Gly Lys Gln Tyr Ser Met Glu Ala Ala Pro Ala Ala Pro Phe
 50 55 60
 Arg Pro Ser Gln Gly Phe Leu Ser Arg Arg Leu Lys Ser Ser Ile Lys
 65 70 75 80
 Arg Thr Lys Ser Gln Pro Lys Leu Asp Arg Thr Ser Ser Phe Arg Gln
 85 90 95

Ile Leu Pro Arg Phe Arg Ser Ala Asp His Asp Arg Ala Arg Leu Met
 100 105 110
 Gln Ser Phe Lys Glu Ser His Ser His Glu Ser Leu Leu Ser Pro Ser
 115 120 125
 Ser Ala Ala Glu Ala Leu Glu Leu Asn Leu Asp Glu Asp Ser Ile Ile
 130 135 140
 Lys Pro Val His Ser Ser Ile Leu Gly Gln Glu Phe Cys Phe Glu Val
 145 150 155 160
 Thr Thr Ser Ser Gly Thr Lys Cys Phe Ala Cys Arg Ser Ala Ala Glu
 165 170 175
 Arg Asp Lys Trp Ile Glu Asn Leu Gln Arg Ala Val Lys Pro Asn Lys
 180 185 190
 Asp Asn Ser Arg Arg Val Asp Asn Val Leu Lys Leu Trp Ile Ile Glu
 195 200 205
 Ala Arg Glu Leu Pro Pro Lys Lys Arg Tyr Tyr Cys Glu Leu Cys Leu
 210 215 220
 Asp Asp Met Leu Tyr Ala Arg Thr Thr Ser Lys Pro Arg Ser Ala Ser
 225 230 235 240
 Gly Asp Thr Val Phe Trp Gly Glu His Phe Glu Phe Asn Asn Leu Pro
 245 250 255
 Ala Val Arg Ala Leu Arg Leu His Leu Tyr Arg Asp Ser Asp Lys Lys
 260 265 270
 Arg Lys Lys Asp Lys Ala Gly Tyr Val Gly Leu Val Thr Val Pro Val
 275 280 285
 Ala Thr Leu Ala Gly Arg His Phe Thr Glu Gln Trp Tyr Pro Val Thr
 290 295 300
 Leu Pro Thr Gly Ser Gly Gly Ser Gly Gly Met Gly Ser Gly Gly Gly
 305 310 315 320
 Gly Gly Ser Gly Gly Gly Ser Gly Gly Lys Gly Lys Gly Gly Cys Pro
 325 330 335
 Ala Val Arg Leu Lys Ala Arg Tyr Gln Thr Met Ser Ile Leu Pro Met
 340 345 350
 Glu Leu Tyr Lys Glu Phe Ala Glu Tyr Val Thr Asn His Tyr Arg Met
 355 360 365
 Leu Cys Ala Val Leu Glu Pro Ala Leu Asn Val Lys Gly Lys Glu Glu
 370 375 380
 Val Ala Ser Ala Leu Val His Ile Leu Gln Ser Thr Gly Lys Ala Lys
 385 390 395 400

Asp Phe Leu Ser Asp Met Ala Met Ser Glu Val Asp Arg Phe Met Glu
 405 410 415
 Arg Glu His Leu Ile Phe Arg Glu Asn Thr Leu Ala Thr Lys Ala Ile
 420 425 430
 Glu Glu Tyr Met Arg Leu Ile Gly Gln Lys Tyr Leu Lys Asp Ala Ile
 435 440 445
 Gly Glu Phe Ile Arg Ala Leu Tyr Glu Ser Glu Glu Asn Cys Glu Val
 450 455 460
 Asp Pro Ile Lys Cys Thr Ala Ser Ser Leu Ala Glu His Gln Ala Asn
 465 470 475 480
 Leu Arg Met Cys Cys Glu Leu Ala Leu Cys Lys Val Val Asn Ser His
 485 490 495
 Cys Val Phe Pro Arg Glu Leu Lys Glu Val Phe Ala Ser Trp Arg Leu
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 Arg Cys Ala Glu Arg Gly Arg Glu Asp Ile Ala Asp Arg Leu Ile Ser
 515 520 525
 Ala Ser Leu Phe Leu Arg Phe Leu Cys Pro Ala Ile Met Ser Pro Ser
 530 535 540
 Leu Phe Gly Leu Met Gln Glu Tyr Pro Asp Glu Gln Thr Ser Arg Thr
 545 550 555 560
 Leu Thr Leu Ile Ala Lys Val Ile Gln Asn Leu Ala Asn Phe Ser Lys
 565 570 575
 Phe Thr Ser Lys Glu Asp Phe Leu Gly Phe Met Asn Glu Phe Leu Glu
 580 585 590
 Leu Glu Trp Gly Ser Met Gln Gln Phe Leu Tyr Glu Ile Ser Asn Leu
 595 600 605
 Asp Thr Leu Thr Asn Ser Ser Ser Phe Glu Gly Tyr Ile Asp Leu Gly
 610 615 620
 Arg Glu Leu Ser Thr Leu His Ala Leu Leu Trp Glu Val Leu Pro Gln
 625 630 635 640
 Leu Ser Lys Glu Ala Leu Leu Lys Leu Gly Pro Leu Pro Arg Leu Leu
 645 650 655
 Ser Asp Ile Ser Thr Ala Leu Arg Asn Pro Asn Ile Gln Arg Gln Pro
 660 665 670
 Ser Arg Gln Ser Glu Arg Ala Arg Ser Gln Pro Met Val Leu Arg Gly
 675 680 685
 Pro Ser Ala Glu Met Gln Gly Tyr Met Met Arg Asp Leu Asn Ser Ser
 690 695 700

Ile Asp Leu Gln Ser Phe Met Ala Arg Gly Leu Asn Ser Ser Met Asp		
705	710	715 720
Met Ala Arg Leu Pro Ser Pro Thr Lys Glu Lys Pro Pro Pro Pro Pro		
	725	730 735
Pro Gly Gly Gly Lys Asp Leu Phe Tyr Val Ser Arg Pro Pro Leu Ala		
	740	745 750
Arg Ser Ser Pro Ala Tyr Cys Thr Ser Ser Ser Asp Ile Thr Glu Pro		
	755	760 765
Glu Gln Lys Met Leu Ser Val Asn Lys Ser Val Ser Met Leu Asp Leu		
	770	775 780
Gln Gly Asp Gly Pro Gly Gly Arg Leu Asn Ser Ser Ser Val Ser Asn		
785	790	795 800
Leu Ala Ala Val Gly Asp Leu Leu His Ser Ser Gln Ala Ser Leu Thr		
	805	810 815
Ala Ala Leu Gly Leu Arg Pro Ala Pro Ala Gly Arg Leu Ser Gln Gly		
	820	825 830
Ser Gly Ser Ser Ile Thr Ala Ala Gly Met Arg Leu Ser Gln Met Gly		
	835	840 845
Val Thr Thr Asp Gly Val Pro Ala Gln Gln Leu Arg Ile Pro Leu Ser		
	850	855 860
Phe Gln Asn Pro Leu Phe His Met Ala Ala Asp Gly Pro Gly Pro Pro		
865	870	875 880
Ala Gly His Gly Gly Ser Ser Gly His Gly Pro Pro Ser Ser His His		
	885	890 895
His His His His His His His His Arg Gly Gly Glu Pro Pro Gly Asp		
	900	905 910
Thr Phe Ala Pro Phe His Gly Tyr Ser Lys Ser Glu Asp Leu Ser Thr		
	915	920 925
Gly Val Pro Lys Pro Pro Ala Ala Ser Ile Leu His Ser His Ser Tyr		
	930	935 940
Ser Asp Glu Phe Gly Pro Ser Gly Thr Asp Phe Thr Arg Arg Gln Leu		
945	950	955 960
Ser Leu Gln Asp Asn Leu Gln His Met Leu Ser Pro Pro Gln Ile Thr		
	965	970 975
Ile Gly Pro Gln Arg Pro Ala Pro Ser Gly Pro Gly Gly Gly Ser Gly		
	980	985 990
Gly Gly Ser Gly Gly Gly Gly Gly Gly Gln Pro Pro Pro Leu Gln Arg		
	995	1000 1005

Gly Lys Ser Gln Gln Leu Thr Val Ser Ala Ala Gln Lys Pro Arg Pro
 1010 1015 1020
 Ser Ser Gly Asn Leu Leu Gln Ser Pro Glu Pro Ser Tyr Gly Pro Ala
 1025 1030 1035 1040
 Arg Pro Arg Gln Gln Ser Leu Ser Lys Glu Gly Ser Ile Gly Gly Ser
 1045 1050 1055
 Gly Gly Ser Gly Gly Gly Gly Gly Gly Leu Lys Pro Ser Ile Thr
 1060 1065 1070
 Lys Gln His Ser Gln Thr Pro Ser Thr Leu Asn Pro Thr Met Pro Ala
 1075 1080 1085
 Ser Glu Arg Thr Val Ala Trp Val Ser Asn Met Pro His Leu Ser Ala
 1090 1095 1100
 Asp Ile Glu Ser Ala His Ile Glu Arg Glu Glu Tyr Lys Leu Lys Glu
 1105 1110 1115 1120
 Tyr Ser Lys Ser Met Asp Glu Ser Arg Leu Asp Arg Val Lys Glu Tyr
 1125 1130 1135
 Glu Glu Glu Ile His Ser Leu Lys Glu Arg Leu His Met Ser Asn Arg
 1140 1145 1150
 Lys Leu Glu Glu Tyr Glu Arg Arg Leu Leu Ser Gln Glu Glu Gln Thr
 1155 1160 1165
 Ser Lys Ile Leu Met Gln Tyr Gln Ala Arg Leu Glu Gln Ser Glu Lys
 1170 1175 1180
 Arg Leu Arg Gln Gln Gln Val Glu Lys Asp Ser Gln Ile Lys Ser Ile
 1185 1190 1195 1200
 Ile Gly Arg Leu Met Leu Val Glu Glu Glu Leu Arg Arg Asp His Pro
 1205 1210 1215
 Ala Met Ala Glu Pro Leu Pro Glu Pro Lys Lys Arg Leu Leu Asp Ala
 1220 1225 1230
 Gln Arg Gly Ser Phe Pro Pro Trp Val Gln Gln Thr Arg Val Arg Trp
 1235 1240 1245
 Pro His Leu Gly Thr Ala Trp Pro Pro Gln Pro His Pro Pro His Pro
 1250 1255 1260
 Gly Cys Arg Ser Gln Arg Thr Ala Ser Ser Gly Thr Pro Gln Thr Thr
 1265 1270 1275 1280
 Ser Pro Pro Ser Ile Thr Asp Leu Leu Pro Cys Ala Pro Tyr Pro Gly
 1285 1290 1295
 Pro Pro Ser Val Thr Asp Leu Leu Pro Ser Ala Pro Asp Pro Gly Thr
 1300 1305 1310

Ser Pro Thr Thr Arg Thr Gly Arg His Gln Gly Thr Ala Gly Leu Ser
 1315 1320 1325

Pro Leu Thr Pro Pro Trp Gly Thr His Leu Ser Thr Pro Leu Leu His
 1330 1335 1340

Ser Arg Arg Glu Ser Gly Thr Leu Ser Cys Pro Leu Thr Pro Gly His
 1345 1350 1355 1360

His Leu Pro His Thr Asp Pro Phe Thr Leu Gly Cys Tyr Pro His Pro
 1365 1370 1375

<210> 5
 <211> 3981
 <212> DNA
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: mammalian
 SYNGAP-C

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 Gly Glu Thr Glu Leu Pro Gln Ala Pro His Phe Pro Phe Ala Pro
 1 5 10 15

cag caa ggc ttc ctg agc cgg agg cta aaa agc tcc atc aaa cgt aca 96
 Gln Gln Gly Phe Leu Ser Arg Arg Leu Lys Ser Ser Ile Lys Arg Thr
 20 25 30

aag tca caa ccc aaa ctt gac cgg acc agc agc ttt cga cag atc ctg 144
 Lys Ser Gln Pro Lys Leu Asp Arg Thr Ser Ser Phe Arg Gln Ile Leu
 35 40 45

cct cgc ttc cga agt gct gac cat gac cgg gcc cgg ctg atg cag agc 192
 Pro Arg Phe Arg Ser Ala Asp His Asp Arg Ala Arg Leu Met Gln Ser
 50 55 60

ttc aag gag tct cac tcc cat gag tcc ctg ctg agt ccc agc agt gct 240
 Phe Lys Glu Ser His Ser His Glu Ser Leu Leu Ser Pro Ser Ser Ala
 65 70 75

gct gag gcc ctg gag ctc aac ctg gat gaa gac tcc att atc aag cca 288
 Ala Glu Ala Leu Glu Leu Asn Leu Asp Glu Asp Ser Ile Ile Lys Pro
 80 85 90 95

gta cac agc tcc atc ctg ggc cag gag ttc tgc ttt gag gta aca aca 336
 Val His Ser Ser Ile Leu Gly Gln Glu Phe Cys Phe Glu Val Thr Thr
 100 105 110

tcg tct ggg aca aaa tgt ttt gcc tgt cgg tct gca gcc gaa agg gac	384
Ser Ser Gly Thr Lys Cys Phe Ala Cys Arg Ser Ala Ala Glu Arg Asp	
115 120 125	
aaa tgg att gag aat cta cag agg gct gtg aaa ccc aac aag gac aac	432
Lys Trp Ile Glu Asn Leu Gln Arg Ala Val Lys Pro Asn Lys Asp Asn	
130 135 140	
agc cgc cgg gta gat aac gtg ctg aaa cta tgg atc ata gaa gct cga	480
Ser Arg Arg Val Asp Asn Val Leu Lys Leu Trp Ile Ile Glu Ala Arg	
145 150 155	
gag ctg ccc ccc aag aag cga tat tac tgc gag tta tgc ctg gac gac	528
Glu Leu Pro Pro Lys Lys Arg Tyr Tyr Cys Glu Leu Cys Leu Asp Asp	
160 165 170 175	
atg ctc tat gca cgg acc act tcc aag ccc cgc tca gcc tca gga gac	576
Met Leu Tyr Ala Arg Thr Thr Ser Lys Pro Arg Ser Ala Ser Gly Asp	
180 185 190	
act gtc ttt tgg ggc gag cac ttc gag ttt aac aac ctg cct gct gtc	624
Thr Val Phe Trp Gly Glu His Phe Glu Phe Asn Asn Leu Pro Ala Val	
195 200 205	
cgg gcg ctg cgg ctg cat ctg tac cgt gac tgc gac aaa aag cgg aag	672
Arg Ala Leu Arg Leu His Leu Tyr Arg Asp Ser Asp Lys Lys Arg Lys	
210 215 220	
aag gac aag gca ggc tac gtt ggc ctg gtg act gtt cca gtg gcc acc	720
Lys Asp Lys Ala Gly Tyr Val Gly Leu Val Thr Val Pro Val Ala Thr	
225 230 235	
ctg gct ggg cgc cac ttc aca gag cag tgg tac ccc gtg acc ctg cca	768
Leu Ala Gly Arg His Phe Thr Glu Gln Trp Tyr Pro Val Thr Leu Pro	
240 245 250 255	
aca gga agt ggg ggc tct ggg ggt atg ggc tgc ggg gga gga ggg ggg	816
Thr Gly Ser Gly Gly Ser Gly Gly Met Gly Ser Gly Gly Gly Gly Gly	
260 265 270	
tca ggg ggc ggc tca ggg ggc aaa ggg aaa gga ggc tgt cct gct gtg	864
Ser Gly Gly Gly Ser Gly Gly Lys Gly Lys Gly Gly Cys Pro Ala Val	
275 280 285	
cgg ctg aag gcc cgt tac cag aca atg agt atc ctg ccc atg gag cta	912
Arg Leu Lys Ala Arg Tyr Gln Thr Met Ser Ile Leu Pro Met Glu Leu	
290 295 300	
tat aag gag ttt gca gaa tat gtg acc aac cac tac cgc atg ctg tgt	960
Tyr Lys Glu Phe Ala Glu Tyr Val Thr Asn His Tyr Arg Met Leu Cys	
305 310 315	
gcc gtg ctg gag ccc gcc ctc aat gtc aag ggc aag gag gag gtc gct	1008
Ala Val Leu Glu Pro Ala Leu Asn Val Lys Gly Lys Glu Glu Val Ala	
320 325 330 335	

agt gca ctg gtt cac atc ctg caa agc aca ggc aag gcc aag gac ttc	1056
Ser Ala Leu Val His Ile Leu Gln Ser Thr Gly Lys Ala Lys Asp Phe	
340 345 350	
ctt tca gac atg gcc atg tca gag gta gac cgg ttc atg gag cgg gaa	1104
Leu Ser Asp Met Ala Met Ser Glu Val Asp Arg Phe Met Glu Arg Glu	
355 360 365	
cac ctc ata ttc cgc gag aac acg ctc gcc act aaa gcc ata gaa gag	1152
His Leu Ile Phe Arg Glu Asn Thr Leu Ala Thr Lys Ala Ile Glu Glu	
370 375 380	
tat atg aga ctg att ggc cag aaa tac ctc aag gat gcc att ggg gag	1200
Tyr Met Arg Leu Ile Gly Gln Lys Tyr Leu Lys Asp Ala Ile Gly Glu	
385 390 395	
ttc atc cgg gct ctg tat gaa tct gag gag aac tgt gaa gta gac ccc	1248
Phe Ile Arg Ala Leu Tyr Glu Ser Glu Glu Asn Cys Glu Val Asp Pro	
400 405 410 415	
atc aag tgc aca gcg tcc agt ctg gca gag cac cag gcc aac ctg cgg	1296
Ile Lys Cys Thr Ala Ser Ser Leu Ala Glu His Gln Ala Asn Leu Arg	
420 425 430	
atg tgc tgt gag ttg gcc ctg tgc aag gtg gtc aac tcc cat tgc gtg	1344
Met Cys Cys Glu Leu Ala Leu Cys Lys Val Val Asn Ser His Cys Val	
435 440 445	
ttc ccg agg gag ctg aag gag gtg ttt gca tca tgg cgg ctg cgc tgt	1392
Phe Pro Arg Glu Leu Lys Glu Val Phe Ala Ser Trp Arg Leu Arg Cys	
450 455 460	
gca gag cgg gcc cgg gag gac att gct gac agg ctg atc agc gcc tcg	1440
Ala Glu Arg Gly Arg Glu Asp Ile Ala Asp Arg Leu Ile Ser Ala Ser	
465 470 475	
ctc ttc ctg cgc ttc ctc tgc ccg gcc atc atg tcg ccc agt ctg ttt	1488
Leu Phe Leu Arg Phe Leu Cys Pro Ala Ile Met Ser Pro Ser Leu Phe	
480 485 490 495	
gga ctg atg cag gag tac cca gat gag cag acc tca cga acc ctc acc	1536
Gly Leu Met Gln Glu Tyr Pro Asp Glu Gln Thr Ser Arg Thr Leu Thr	
500 505 510	
ctc atc gcc aag gtt atc cag aac ctg gcc aac ttt tcc aag ttt acc	1584
Leu Ile Ala Lys Val Ile Gln Asn Leu Ala Asn Phe Ser Lys Phe Thr	
515 520 525	
tca aag gag gac ttc ctg gcc ttc atg aac gag ttt ctg gag ctg gaa	1632
Ser Lys Glu Asp Phe Leu Gly Phe Met Asn Glu Phe Leu Glu Leu Glu	
530 535 540	
tgg ggt tct atg cag caa ttc ttg tat gag ata tcc aac ctg gac aca	1680
Trp Gly Ser Met Gln Gln Phe Leu Tyr Glu Ile Ser Asn Leu Asp Thr	
545 550 555	

ctg acc aac agc agc agt ttt gag ggc tac ata gac ttg ggc cgc gag Leu Thr Asn Ser Ser Ser Phe Glu Gly Tyr Ile Asp Leu Gly Arg Glu 560 565 570 575	1728
ctc tcc aca ctt cac gcc ctg ctc tgg gag gtg ctg ccc cag ctc agc Leu Ser Thr Leu His Ala Leu Leu Trp Glu Val Leu Pro Gln Leu Ser 580 585 590	1776
aag gaa gcc ctc ctg aag ctg ggc ccg ctg ccc cgg ctc ctc agc gac Lys Glu Ala Leu Leu Lys Leu Gly Pro Leu Pro Arg Leu Leu Ser Asp 595 600 605	1824
atc agc aca gcc ctg agg aac cct aac atc caa agg cag ccg agc cgc Ile Ser Thr Ala Leu Arg Asn Pro Asn Ile Gln Arg Gln Pro Ser Arg 610 615 620	1872
cag agc gag cgc gct cgg tct cag ccc atg gtg ctg cgc ggg ccg tca Gln Ser Glu Arg Ala Arg Ser Gln Pro Met Val Leu Arg Gly Pro Ser 625 630 635	1920
gcc gaa atg cag ggc tac atg atg cgg gac ctc aac agc tcc atc gac Ala Glu Met Gln Gly Tyr Met Met Arg Asp Leu Asn Ser Ser Ile Asp 640 645 650 655	1968
ctt cag tcc ttc atg gct cga ggc ctc aac agc tct atg gac atg gct Leu Gln Ser Phe Met Ala Arg Gly Leu Asn Ser Ser Met Asp Met Ala 660 665 670	2016
cgc ctc ccc tcc cca acc aag gag aaa ccc ccg ccg ccc cct ccc ggt Arg Leu Pro Ser Pro Thr Lys Glu Lys Pro Pro Pro Pro Pro Pro Gly 675 680 685	2064
ggg ggt aaa gac ctg ttc tat gtg agc cgg cca cca ctg gcc cgg tcc Gly Gly Lys Asp Leu Phe Tyr Val Ser Arg Pro Pro Leu Ala Arg Ser 690 695 700	2112
tcc cca gca tac tgc acg agc agc tcg gac atc aca gag ccg gag cag Ser Pro Ala Tyr Cys Thr Ser Ser Ser Asp Ile Thr Glu Pro Glu Gln 705 710 715	2160
aag atg ctg agt gtc aac aag agt gtg tcc atg ctg gac ctg cag ggc Lys Met Leu Ser Val Asn Lys Ser Val Ser Met Leu Asp Leu Gln Gly 720 725 730 735	2208
gac ggg cct ggg ggc cgc ctt aac agc agt agt gtt tcc aac ctg gca Asp Gly Pro Gly Gly Arg Leu Asn Ser Ser Ser Val Ser Asn Leu Ala 740 745 750	2256
gct gtt ggg gac ctg ttg cac tca agc cag gct tca ctg aca gca gcc Ala Val Gly Asp Leu Leu His Ser Ser Gln Ala Ser Leu Thr Ala Ala 755 760 765	2304
ttg ggg ttg cgg cct gca cct gcc ggg cgc ctc tcc caa ggg agt ggc Leu Gly Leu Arg Pro Ala Pro Ala Gly Arg Leu Ser Gln Gly Ser Gly 770 775 780	2352

tct tcc atc aca gca gcc ggc atg cgc ctc agc cag atg ggt gtc act Ser Ser Ile Thr Ala Ala Gly Met Arg Leu Ser Gln Met Gly Val Thr 785 790 795	2400
acg gat ggt gtc ccc gcc cag caa ctg cgc atc cct ctt tcc ttc cag Thr Asp Gly Val Pro Ala Gln Gln Leu Arg Ile Pro Leu Ser Phe Gln 800 805 810 815	2448
aac cct ctc ttc cat atg gct gcc gat gga cca ggg ccc cca gca ggc Asn Pro Leu Phe His Met Ala Ala Asp Gly Pro Gly Pro Pro Ala Gly 820 825 830	2496
cat gga ggg agc agt ggc cat ggt cca cct tcc tcc cat cac cac cac His Gly Gly Ser Ser Gly His Gly Pro Pro Ser Ser His His His His 835 840 845	2544
cac cac cat cac cat cac cga ggg gga gaa ccc cca ggg gac act ttt His His His His His His Arg Gly Glu Pro Pro Gly Asp Thr Phe 850 855 860	2592
gcc ccg ttc cat ggc tat agc aag agc gag gac ctc tct aca ggg gtc Ala Pro Phe His Gly Tyr Ser Lys Ser Glu Asp Leu Ser Thr Gly Val 865 870 875	2640
cct aag ccc cct gcg gcc tcc atc ctt cac agc cac agc tac agt gat Pro Lys Pro Pro Ala Ala Ser Ile Leu His Ser His Ser Tyr Ser Asp 880 885 890 895	2688
gag ttt gga ccc tct ggt act gat ttt acc cgt cgg cag ctc tca ctt Glu Phe Gly Pro Ser Gly Thr Asp Phe Thr Arg Arg Gln Leu Ser Leu 900 905 910	2736
cag gac aac cta cag cac atg ctc tcc ccg ccc cag atc acc atc ggt Gln Asp Asn Leu Gln His Met Leu Ser Pro Pro Gln Ile Thr Ile Gly 915 920 925	2784
ccc cag agg cca gct ccc tca ggg cca gga ggg ggc agt ggt ggg ggc Pro Gln Arg Pro Ala Pro Ser Gly Pro Gly Gly Gly Ser Gly Gly Gly 930 935 940	2832
agt ggt ggg ggc ggt ggg ggc cag cca cct ccc ttg cag agg ggc aaa Ser Gly Gly Gly Gly Gly Gly Gln Pro Pro Pro Leu Gln Arg Gly Lys 945 950 955	2880
tct cag cag ttg aca gtg agt gct gcc cag aaa ccc cgg ccg tcc agc Ser Gln Gln Leu Thr Val Ser Ala Ala Gln Lys Pro Arg Pro Ser Ser 960 965 970 975	2928
ggg aac cta ttg cag tcc ccg gaa cca agt tat ggt cct gcc cgt cca Gly Asn Leu Leu Gln Ser Pro Glu Pro Ser Tyr Gly Pro Ala Arg Pro 980 985 990	2976
cgg caa cag agc ctc agc aaa gag ggc agc att ggg ggc agc ggg ggc Arg Gln Gln Ser Leu Ser Lys Glu Gly Ser Ile Gly Gly Ser Gly Gly 995 1000 1005	3024

agc ggt ggc gga ggg ggt ggg ggg ctc aag ccc tcc atc acc aag cag Ser Gly Gly Gly Gly Gly Gly Gly Leu Lys Pro Ser Ile Thr Lys Gln 1010 1015 1020	3072
cat tcc cag act cca tcc acg ctg aac ccc acg atg ccg gcc tcg gag His Ser Gln Thr Pro Ser Thr Leu Asn Pro Thr Met Pro Ala Ser Glu 1025 1030 1035	3120
cgg act gta gcc tgg gtg tcc aat atg cct cac ctg tcc gct gac atc Arg Thr Val Ala Trp Val Ser Asn Met Pro His Leu Ser Ala Asp Ile 1040 1045 1050 1055	3168
gag agt gca cac att gag cgg gaa gag tac aag ctg aag gag tac tcg Glu Ser Ala His Ile Glu Arg Glu Glu Tyr Lys Leu Lys Glu Tyr Ser 1060 1065 1070	3216
aag tcc atg gac gag agc cga ctg gac agg gtg aag gag tac gag gag Lys Ser Met Asp Glu Ser Arg Leu Asp Arg Val Lys Glu Tyr Glu Glu 1075 1080 1085	3264
gag atc cac tca ctg aag gaa agg cta cac atg tcc aac cgg aag ctg Glu Ile His Ser Leu Lys Glu Arg Leu His Met Ser Asn Arg Lys Leu 1090 1095 1100	3312
gaa gag tac gag cgg agg ctg ctg tcc cag gaa gag cag acc agc aag Glu Glu Tyr Glu Arg Arg Leu Leu Ser Gln Glu Glu Gln Thr Ser Lys 1105 1110 1115	3360
atc ctg atg cag tac caa gcc cgc ctg gag cag agc gag aag cgc ttg Ile Leu Met Gln Tyr Gln Ala Arg Leu Glu Gln Ser Glu Lys Arg Leu 1120 1125 1130 1135	3408
agg cag cag cag gtg gag aag gac tcc cag atc aag agc atc att ggc Arg Gln Gln Gln Val Glu Lys Asp Ser Gln Ile Lys Ser Ile Ile Gly 1140 1145 1150	3456
agg ctg atg ctg gtg gag gag gag ctg cgc cgg gac cac ccc gcc atg Arg Leu Met Leu Val Glu Glu Glu Leu Arg Arg Asp His Pro Ala Met 1155 1160 1165	3504
gct gag ccg ctg cct gaa ccc aag aag agg ctg ctc gac gct cag aga Ala Glu Pro Leu Pro Glu Pro Lys Lys Arg Leu Leu Asp Ala Gln Arg 1170 1175 1180	3552
ggc agc ttc ccc cct tgg gtc caa caa acc cgc gtg tga cgc tgg ccc Gly Ser Phe Pro Pro Trp Val Gln Gln Thr Arg Val Arg Trp Pro 1185 1190 1195	3600
cac ctt gga acg gcc tgg ccc ccc cag ccc cac ccc ccc cac ccc ggc His Leu Gly Thr Ala Trp Pro Pro Gln Pro His Pro Pro His Pro Gly 1200 1205 1210	3648
tgc aga tca cag aga acg gcg agt tcc gga aca ccg cag acc act agc Cys Arg Ser Gln Arg Thr Ala Ser Ser Gly Thr Pro Gln Thr Thr Ser 1215 1220 1225 1230	3696

cca ccc agc atc aca gac ctc ctt ccc tgt gca ccc tac ccc ggc cca 3744
 Pro Pro Ser Ile Thr Asp Leu Leu Pro Cys Ala Pro Tyr Pro Gly Pro
 1235 1240 1245

ccc agc gtc aca gac ctc ctt ccc agt gca ccc gac cct gga aca tca 3792
 Pro Ser Val Thr Asp Leu Leu Pro Ser Ala Pro Asp Pro Gly Thr Ser
 1250 1255 1260

cca acc acc agg act gga cgt cac caa ggg aca gcg gga ttg tct ccc 3840
 Pro Thr Thr Arg Thr Gly Arg His Gln Gly Thr Ala Gly Leu Ser Pro
 1265 1270 1275

tta acg cct cct tgg ggc acc cat ctg tca acc cca ctg ctc cat tcc 3888
 Leu Thr Pro Pro Trp Gly Thr His Leu Ser Thr Pro Leu Leu His Ser
 1280 1285 1290

agg agg gag agt ggg acc ctc agc tgc cct ctc acc cca gga cac cac 3936
 Arg Arg Glu Ser Gly Thr Leu Ser Cys Pro Leu Thr Pro Gly His His
 1295 1300 1305 1310

cta ccc cac aca gac ccc ttc act ctg ggg tgc tat ccc cat cct 3981
 Leu Pro His Thr Asp Pro Phe Thr Leu Gly Cys Tyr Pro His Pro
 1315 1320 1325

<210> 6

<211> 1325

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: mammalian
 SYNGAP-C

<400> 6

Gly Glu Thr Glu Leu Pro Gln Ala Pro His Phe Pro Phe Ala Pro Gln
 1 5 10 15

Gln Gly Phe Leu Ser Arg Arg Leu Lys Ser Ser Ile Lys Arg Thr Lys
 20 25 30

Ser Gln Pro Lys Leu Asp Arg Thr Ser Ser Phe Arg Gln Ile Leu Pro
 35 40 45

Arg Phe Arg Ser Ala Asp His Asp Arg Ala Arg Leu Met Gln Ser Phe
 50 55 60

Lys Glu Ser His Ser His Glu Ser Leu Leu Ser Pro Ser Ser Ala Ala
 65 70 75 80

Glu Ala Leu Glu Leu Asn Leu Asp Glu Asp Ser Ile Ile Lys Pro Val
 85 90 95

His Ser Ser Ile Leu Gly Gln Glu Phe Cys Phe Glu Val Thr Thr Ser
 100 105 110

Ser Gly Thr Lys Cys Phe Ala Cys Arg Ser Ala Ala Glu Arg Asp Lys
 115 120 125

Trp Ile Glu Asn Leu Gln Arg Ala Val Lys Pro Asn Lys Asp Asn Ser
 130 135 140
 Arg Arg Val Asp Asn Val Leu Lys Leu Trp Ile Ile Glu Ala Arg Glu
 145 150 155 160
 Leu Pro Pro Lys Lys Arg Tyr Tyr Cys Glu Leu Cys Leu Asp Asp Met
 165 170 175
 Leu Tyr Ala Arg Thr Thr Ser Lys Pro Arg Ser Ala Ser Gly Asp Thr
 180 185 190
 Val Phe Trp Gly Glu His Phe Glu Phe Asn Asn Leu Pro Ala Val Arg
 195 200 205
 Ala Leu Arg Leu His Leu Tyr Arg Asp Ser Asp Lys Lys Arg Lys Lys
 210 215 220
 Asp Lys Ala Gly Tyr Val Gly Leu Val Thr Val Pro Val Ala Thr Leu
 225 230 235 240
 Ala Gly Arg His Phe Thr Glu Gln Trp Tyr Pro Val Thr Leu Pro Thr
 245 250 255
 Gly Ser Gly Gly Ser Gly Gly Met Gly Ser Gly Gly Gly Gly Gly Ser
 260 265 270
 Gly Gly Gly Ser Gly Gly Lys Gly Lys Gly Gly Cys Pro Ala Val Arg
 275 280 285
 Leu Lys Ala Arg Tyr Gln Thr Met Ser Ile Leu Pro Met Glu Leu Tyr
 290 295 300
 Lys Glu Phe Ala Glu Tyr Val Thr Asn His Tyr Arg Met Leu Cys Ala
 305 310 315 320
 Val Leu Glu Pro Ala Leu Asn Val Lys Gly Lys Glu Glu Val Ala Ser
 325 330 335
 Ala Leu Val His Ile Leu Gln Ser Thr Gly Lys Ala Lys Asp Phe Leu
 340 345 350
 Ser Asp Met Ala Met Ser Glu Val Asp Arg Phe Met Glu Arg Glu His
 355 360 365
 Leu Ile Phe Arg Glu Asn Thr Leu Ala Thr Lys Ala Ile Glu Glu Tyr
 370 375 380
 Met Arg Leu Ile Gly Gln Lys Tyr Leu Lys Asp Ala Ile Gly Glu Phe
 385 390 395 400
 Ile Arg Ala Leu Tyr Glu Ser Glu Glu Asn Cys Glu Val Asp Pro Ile
 405 410 415
 Lys Cys Thr Ala Ser Ser Leu Ala Glu His Gln Ala Asn Leu Arg Met
 420 425 430

Cys Cys Glu Leu Ala Leu Cys Lys Val Val Asn Ser His Cys Val Phe
 435 440 445
 Pro Arg Glu Leu Lys Glu Val Phe Ala Ser Trp Arg Leu Arg Cys Ala
 450 455 460
 Glu Arg Gly Arg Glu Asp Ile Ala Asp Arg Leu Ile Ser Ala Ser Leu
 465 470 475 480
 Phe Leu Arg Phe Leu Cys Pro Ala Ile Met Ser Pro Ser Leu Phe Gly
 485 490 495
 Leu Met Gln Glu Tyr Pro Asp Glu Gln Thr Ser Arg Thr Leu Thr Leu
 500 505 510
 Ile Ala Lys Val Ile Gln Asn Leu Ala Asn Phe Ser Lys Phe Thr Ser
 515 520 525
 Lys Glu Asp Phe Leu Gly Phe Met Asn Glu Phe Leu Glu Leu Glu Trp
 530 535 540
 Gly Ser Met Gln Gln Phe Leu Tyr Glu Ile Ser Asn Leu Asp Thr Leu
 545 550 555 560
 Thr Asn Ser Ser Ser Phe Glu Gly Tyr Ile Asp Leu Gly Arg Glu Leu
 565 570 575
 Ser Thr Leu His Ala Leu Leu Trp Glu Val Leu Pro Gln Leu Ser Lys
 580 585 590
 Glu Ala Leu Leu Lys Leu Gly Pro Leu Pro Arg Leu Leu Ser Asp Ile
 595 600 605
 Ser Thr Ala Leu Arg Asn Pro Asn Ile Gln Arg Gln Pro Ser Arg Gln
 610 615 620
 Ser Glu Arg Ala Arg Ser Gln Pro Met Val Leu Arg Gly Pro Ser Ala
 625 630 635 640
 Glu Met Gln Gly Tyr Met Met Arg Asp Leu Asn Ser Ser Ile Asp Leu
 645 650 655
 Gln Ser Phe Met Ala Arg Gly Leu Asn Ser Ser Met Asp Met Ala Arg
 660 665 670
 Leu Pro Ser Pro Thr Lys Glu Lys Pro Pro Pro Pro Pro Gly Gly
 675 680 685
 Gly Lys Asp Leu Phe Tyr Val Ser Arg Pro Pro Leu Ala Arg Ser Ser
 690 695 700
 Pro Ala Tyr Cys Thr Ser Ser Ser Asp Ile Thr Glu Pro Glu Gln Lys
 705 710 715 720
 Met Leu Ser Val Asn Lys Ser Val Ser Met Leu Asp Leu Gln Gly Asp
 725 730 735

Gly Pro Gly Gly Arg Leu Asn Ser Ser Ser Val Ser Asn Leu Ala Ala
 740 745 750
 Val Gly Asp Leu Leu His Ser Ser Gln Ala Ser Leu Thr Ala Ala Leu
 755 760 765
 Gly Leu Arg Pro Ala Pro Ala Gly Arg Leu Ser Gln Gly Ser Gly Ser
 770 775 780
 Ser Ile Thr Ala Ala Gly Met Arg Leu Ser Gln Met Gly Val Thr Thr
 785 790 795 800
 Asp Gly Val Pro Ala Gln Gln Leu Arg Ile Pro Leu Ser Phe Gln Asn
 805 810 815
 Pro Leu Phe His Met Ala Ala Asp Gly Pro Gly Pro Pro Ala Gly His
 820 825 830
 Gly Gly Ser Ser Gly His Gly Pro Pro Ser Ser His His His His His
 835 840 845
 His His His His His Arg Gly Gly Glu Pro Pro Gly Asp Thr Phe Ala
 850 855 860
 Pro Phe His Gly Tyr Ser Lys Ser Glu Asp Leu Ser Thr Gly Val Pro
 865 870 875 880
 Lys Pro Pro Ala Ala Ser Ile Leu His Ser His Ser Tyr Ser Asp Glu
 885 890 895
 Phe Gly Pro Ser Gly Thr Asp Phe Thr Arg Arg Gln Leu Ser Leu Gln
 900 905 910
 Asp Asn Leu Gln His Met Leu Ser Pro Pro Gln Ile Thr Ile Gly Pro
 915 920 925
 Gln Arg Pro Ala Pro Ser Gly Pro Gly Gly Gly Ser Gly Gly Gly Ser
 930 935 940
 Gly Gly Gly Gly Gly Gly Gln Pro Pro Pro Leu Gln Arg Gly Lys Ser
 945 950 955 960
 Gln Gln Leu Thr Val Ser Ala Ala Gln Lys Pro Arg Pro Ser Ser Gly
 965 970 975
 Asn Leu Leu Gln Ser Pro Glu Pro Ser Tyr Gly Pro Ala Arg Pro Arg
 980 985 990
 Gln Gln Ser Leu Ser Lys Glu Gly Ser Ile Gly Gly Ser Gly Gly Ser
 995 1000 1005
 Gly Gly Gly Gly Gly Gly Gly Leu Lys Pro Ser Ile Thr Lys Gln His
 1010 1015 1020
 Ser Gln Thr Pro Ser Thr Leu Asn Pro Thr Met Pro Ala Ser Glu Arg
 1025 1030 1035 1040

Thr Val Ala Trp Val Ser Asn Met Pro His Leu Ser Ala Asp Ile Glu
 1045 1050 1055
 Ser Ala His Ile Glu Arg Glu Glu Tyr Lys Leu Lys Glu Tyr Ser Lys
 1060 1065 1070
 Ser Met Asp Glu Ser Arg Leu Asp Arg Val Lys Glu Tyr Glu Glu Glu
 1075 1080 1085
 Ile His Ser Leu Lys Glu Arg Leu His Met Ser Asn Arg Lys Leu Glu
 1090 1095 1100
 Glu Tyr Glu Arg Arg Leu Leu Ser Gln Glu Glu Gln Thr Ser Lys Ile
 1105 1110 1115 1120
 Leu Met Gln Tyr Gln Ala Arg Leu Glu Gln Ser Glu Lys Arg Leu Arg
 1125 1130 1135
 Gln Gln Gln Val Glu Lys Asp Ser Gln Ile Lys Ser Ile Ile Gly Arg
 1140 1145 1150
 Leu Met Leu Val Glu Glu Glu Leu Arg Arg Asp His Pro Ala Met Ala
 1155 1160 1165
 Glu Pro Leu Pro Glu Pro Lys Lys Arg Leu Leu Asp Ala Gln Arg Gly
 1170 1175 1180
 Ser Phe Pro Pro Trp Val Gln Gln Thr Arg Val Arg Trp Pro His Leu
 1185 1190 1195 1200
 Gly Thr Ala Trp Pro Pro Gln Pro His Pro Pro His Pro Gly Cys Arg
 1205 1210 1215
 Ser Gln Arg Thr Ala Ser Ser Gly Thr Pro Gln Thr Thr Ser Pro Pro
 1220 1225 1230
 Ser Ile Thr Asp Leu Leu Pro Cys Ala Pro Tyr Pro Gly Pro Pro Ser
 1235 1240 1245
 Val Thr Asp Leu Leu Pro Ser Ala Pro Asp Pro Gly Thr Ser Pro Thr
 1250 1255 1260
 Thr Arg Thr Gly Arg His Gln Gly Thr Ala Gly Leu Ser Pro Leu Thr
 1265 1270 1275 1280
 Pro Pro Trp Gly Thr His Leu Ser Thr Pro Leu Leu His Ser Arg Arg
 1285 1290 1295
 Glu Ser Gly Thr Leu Ser Cys Pro Leu Thr Pro Gly His His Leu Pro
 1300 1305 1310
 His Thr Asp Pro Phe Thr Leu Gly Cys Tyr Pro His Pro
 1315 1320 1325

<210> 7

<211> 216

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: mammalian
SYNGAP-C

<400> 7

Gly Lys Ala Lys Asp Phe Leu Ser Asp Met Ala Met Ser Glu Val Asp
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 20 25 30
 Thr Lys Ala Ile Glu Glu Tyr Met Arg Leu Ile Gly Gln Lys Tyr Leu
 35 40 45
 Lys Asp Ala Ile Gly Glu Phe Ile Arg Ala Leu Tyr Glu Ser Glu Glu
 50 55 60
 Asn Cys Glu Val Asp Pro Ile Lys Cys Thr Ala Ser Ser Leu Ala Glu
 65 70 75 80
 His Gln Ala Asn Leu Arg Met Cys Cys Glu Leu Ala Leu Cys Lys Val
 85 90 95
 Val Asn Ser His Cys Val Phe Pro Arg Glu Leu Lys Glu Val Phe Ala
 100 105 110
 Ser Trp Arg Leu Arg Cys Ala Glu Arg Gly Arg Glu Asp Ile Ala Asp
 115 120 125
 Arg Leu Ile Ser Ala Ser Leu Phe Leu Arg Phe Leu Cys Pro Ala Ile
 130 135 140
 Met Ser Pro Ser Leu Phe Gly Leu Met Gln Glu Tyr Pro Asp Glu Gln
 145 150 155 160
 Thr Ser Arg Thr Leu Thr Leu Ile Ala Lys Val Ile Gln Asn Leu Ala
 165 170 175
 Asn Phe Ser Lys Phe Thr Ser Lys Glu Asp Phe Leu Gly Phe Met Asn
 180 185 190
 Glu Phe Leu Glu Leu Glu Trp Gly Ser Met Gln Gln Phe Leu Tyr Glu
 195 200 205
 Ile Ser Asn Leu Asp Thr Leu Thr
 210 215

<210> 8

<211> 218

<212> PRT

<213> Rattus norvegicus

<400> 8

Lys Leu Glu Ser Leu Leu Leu Cys Thr Leu Asn Asp Arg Glu Ile Ser
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 Met Glu Asp Glu Ala Thr Thr Leu Phe Arg Ala Thr Thr Leu Ala Ser
 20 25 30
 Thr Leu Met Glu Gln Tyr Met Lys Ala Thr Ala Thr Gln Phe Val His
 35 40 45
 His Ala Leu Lys Asp Ser Ile Leu Lys Ile Met Glu Val Gln His Lys
 50 55 60
 Trp Pro Thr Asn Asn Thr Met Arg Thr Arg Val Val Ser Gly Phe Val
 65 70 75 80
 Phe Leu Arg Leu Ile Cys Pro Ala Ile Leu Asn Pro Arg Met Phe Asn
 85 90 95
 Ile Ile Ser Asp Ser Pro Ser Pro Ile Ala Ala Arg Thr Leu Thr Leu
 100 105 110
 Val Ala Lys Ser Val Gln Asn Leu Ala Asn Ser Lys Gln Ser Cys Glu
 115 120 125
 Leu Ser Pro Ser Lys Leu Glu Lys Asn Glu Asp Val Asn Thr Asn Leu
 130 135 140
 Ala His Leu Leu Ser Ile Leu Ser Glu Leu Val Glu Lys Ile Phe Met
 145 150 155 160
 Ala Ser Glu Ile Leu Pro Pro Thr Leu Arg Tyr Ile Tyr Gly Cys Leu
 165 170 175
 Gln Lys Ser Leu Val Glu Phe Gly Ala Lys Glu Pro Tyr Met Glu Gly
 180 185 190
 Val Asn Pro Phe Ile Lys Ser Asn Lys His Arg Met Ile Met Phe Leu
 195 200 205
 Asp Glu Leu Gly Asn Val Pro Glu Leu Pro
 210 215

<210> 9

<211> 219

<212> PRT

<213> Homo sapiens

<400> 9

His Leu Leu Tyr Gln Leu Leu Trp Asn Met Phe Ser Lys Glu Val Glu
 1 5 10 15
 Leu Ala Asp Ser Met Gln Thr Leu Phe Arg Gly Asn Ser Leu Ala Ser
 20 25 30
 Lys Ile Met Thr Phe Cys Phe Lys Val Tyr Gly Ala Thr Tyr Leu Gln
 35 40 45

Lys Leu Leu Asp Pro Leu Leu Arg Ile Val Ile Thr Ser Ser Asp Trp
 50 55 60
 Gln His Val Ser Phe Glu Val Asp Pro Thr Arg Leu Glu Pro Ser Glu
 65 70 75 80
 Ser Leu Glu Glu Asn Gln Arg Asn Leu Leu Gln Met Thr Glu Lys Phe
 85 90 95
 Phe His Ala Ile Ile Ser Ser Ser Ser Glu Phe Pro Pro Gln Leu Arg
 100 105 110
 Ser Val Cys His Cys Leu Tyr Gln Val Val Ser Gln Arg Phe Pro Gln
 115 120 125
 Asn Ser Ile Gly Ala Val Gly Ser Ala Met Phe Leu Arg Phe Ile Asn
 130 135 140
 Pro Ala Ile Val Ser Pro Tyr Glu Ala Gly Ile Leu Asp Lys Lys Pro
 145 150 155 160
 Pro Pro Arg Ile Glu Arg Gly Leu Lys Leu Met Ser Lys Ile Leu Gln
 165 170 175
 Ser Ile Ala Asn His Val Leu Phe Thr Lys Glu Glu His Met Arg Pro
 180 185 190
 Phe Asn Asp Phe Val Lys Ser Asn Phe Asp Ala Ala Arg Arg Phe Phe
 195 200 205
 Leu Asp Ile Ala Ser Asp Cys Pro Thr Ser Asp
 210 215

<210> 10

<211> 82

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: mammalian
 SYNGAP-A

<400> 10

Phe Lys Glu Ser His Ser His Glu Ser Leu Leu Ser Pro Ser Ser Ala
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 Ala Glu Ala Leu Glu Leu Asn Leu Asp Glu Asp Ser Ile Lys Lys Pro
 20 25 30
 Val His Ser Ser Ile Leu Gly Gln Glu Phe Cys Phe Glu Val Thr Thr
 35 40 45
 Ser Ser Gly Thr Lys Cys Phe Ala Cys Arg Ser Ala Ala Glu Arg Asp
 50 55 60

Lys Trp Ile Glu Asn Leu Gln Arg Ala Val Lys Pro Asn Lys Asp Asn
 65 70 75 80

Ser Arg

<210> 11
 <211> 114
 <212> PRT
 <213> Homo sapiens

<400> 11
 Phe Tyr Lys Asn Ile Val Lys Lys Gly Tyr Leu Leu Lys Lys Gly Lys
 1 5 10 15
 Gly Lys Arg Trp Lys Asn Leu Tyr Phe Ile Leu Glu Gly Ser Asp Ala
 20 25 30
 Gln Leu Ile Tyr Phe Glu Ser Glu Lys Arg Ala Thr Lys Pro Lys Gly
 35 40 45
 Leu Ile Asp Leu Ser Val Cys Ser Val Tyr Val Val His Asp Ser Leu
 50 55 60
 Phe Gly Arg Pro Asn Cys Phe Gln Ile Val Val Gln His Phe Ser Glu
 65 70 75 80
 Glu His Tyr Ile Phe Tyr Phe Ala Gly Glu Thr Pro Glu Gln Ala Glu
 85 90 95
 Asp Trp Met Lys Gly Leu Gln Ala Phe Cys Asn Leu Arg Lys Ser Ser
 100 105 110

Pro Gly

<210> 12
 <211> 111
 <212> PRT
 <213> Drosophila melanogaster

<400> 12
 Pro Val Leu Leu Lys Glu Gly Glu Gly Leu Met Thr Lys Tyr Pro Thr
 1 5 10 15
 Ser Arg Lys Arg Phe Gly Arg Gln Phe Lys Gln Arg His Phe Arg Leu
 20 25 30
 Thr Thr His Ser Leu Ser Tyr Ala Lys Ser Lys Gly Lys Gln Pro Ile
 35 40 45
 Cys Asp Ile Pro Leu Gln Glu Ile Ala Ser Val Glu Gln Leu Lys Asp
 50 55 60
 Lys Ser Phe Lys Met Gln Asn Cys Phe Lys Ile Val His Asn Asp Arg
 65 70 75 80

Ser Leu Ile Val Gln Thr Thr Asn Cys Val Glu Glu Arg Glu Trp Phe
 85 90 95

Asp Leu Leu His Lys Ile Cys Leu Met Asn Ser Ile Arg Met Gln
 100 105 110

<210> 13

<211> 108

<212> PRT

<213> Homo sapiens

<400> 13

Met Glu Pro Lys Arg Ile Arg Glu Gly Tyr Leu Val Lys Lys Gly Ser
 1 5 10 15

Val Phe Asn Thr Trp Lys Pro Met Trp Val Val Leu Leu Glu Asp Gly
 20 25 30

Ile Glu Phe Tyr Lys Lys Lys Ser Asp Asn Ser Pro Lys Gly Met Ile
 35 40 45

Pro Leu Lys Gly Ser Thr Leu Thr Ser Pro Cys Gln Asp Phe Gly Lys
 50 55 60

Arg Met Phe Val Phe Lys Ile Thr Thr Thr Lys Gln Gln Asp His Phe
 65 70 75 80

Phe Gln Ala Ala Phe Leu Glu Glu Arg Asp Ala Trp Val Arg Asp Ile
 85 90 95

Asn Lys Ala Ile Lys Cys Ile Glu Gly Gly Gln Lys
 100 105

<210> 14

<211> 110

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: mammalian
 SYNGAP-A

<400> 14

Val Asp Asn Val Leu Lys Leu Trp Ile Ile Glu Ala Arg Glu Leu Pro
 1 5 10 15

Pro Lys Lys Arg Tyr Tyr Cys Glu Leu Cys Leu Asp Asp Met Leu Tyr
 20 25 30

Ala Arg Thr Thr Ser Lys Pro Arg Ser Ala Ser Gly Asp Thr Val Phe
 35 40 45

Trp Gly Glu His Phe Glu Phe Asn Asn Leu Pro Ala Val Arg Ala Leu
 50 55 60

Arg Leu His Leu Tyr Arg Asp Ser Asp Lys Lys Arg Lys Lys Asp Lys
65 70 75 80

Ala Gly Tyr Val Gly Leu Val Thr Val Pro Val Ala Thr Leu Ala Gly
85 90 95

Arg His Phe Thr Glu Gln Trp Tyr Pro Val Thr Leu Pro Thr
100 105 110

<210> 15
<211> 107
<212> PRT
<213> Homo sapiens

<400> 15
Gln Val Ser Ser Leu Val Leu His Ile Glu Glu Ala His Lys Leu Pro
1 5 10 15

Val Lys His Phe Thr Asn Pro Tyr Cys Asn Ile Tyr Leu Asn Ser Val
20 25 30

Gln Val Ala Lys Thr His Ala Arg Glu Gly Gln Asn Pro Val Trp Ser
35 40 45

Glu Glu Phe Val Phe Asp Asp Leu Pro Pro Asp Ile Asn Arg Phe Glu
50 55 60

Ile Thr Leu Ser Asn Lys Thr Lys Lys Ser Lys Asp Pro Asp Ile Leu
65 70 75 80

Phe Met Arg Cys Gln Leu Ser Arg Leu Gln Lys Gly His Ala Thr Asp
85 90 95

Glu Trp Phe Leu Leu Ser Ser His Ile Pro Leu
100 105

<210> 16
<211> 116
<212> PRT
<213> Rattus norvegicus

<400> 16
Asp Tyr Asp Phe Gln Ala Asn Gln Leu Thr Val Gly Val Leu Gln Ala
1 5 10 15

Ala Glu Leu Pro Ala Leu Asp Met Gly Gly Thr Ser Asp Pro Tyr Val
20 25 30

Lys Val Phe Leu Leu Pro Asp Lys Lys Lys Lys Tyr Glu Thr Lys Val
35 40 45

His Arg Lys Thr Leu Asn Pro Ala Phe Asn Glu Thr Phe Thr Phe Lys
50 55 60

Val Pro Tyr Gln Glu Leu Gly Gly Lys Thr Leu Val Met Ala Ile Tyr
65 70 75 80

Asp Phe Asp Arg Phe Ser Lys His Asp Ile Ile Gly Glu Val Lys Val
85 90 95

Pro Met Asn Thr Val Asp Leu Gly Gln Pro Ile Glu Glu Trp Arg Asp
100 105 110

Leu Gln Gly Gly
115

<210> 17

<211> 132

<212> PRT

<213> Bos taurus

<400> 17

Leu Tyr Asp Gln Asp Asn Ser Ser Leu Lys Cys Thr Ile Ile Lys Ala
1 5 10 15

Lys Gly Leu Lys Pro Met Asp Ser Asn Gly Leu Ala Asp Pro Tyr Val
20 25 30

Lys Leu His Leu Leu Pro Gly Ala Ser Lys Ser Asn Lys Leu Arg Thr
35 40 45

Lys Thr Leu Arg Asn Thr Arg Asn Pro Ile Trp Asn Glu Thr Leu Val
50 55 60

Tyr His Gly Ile Thr Asp Glu Asp Met Gln Arg Lys Thr Leu Arg Ile
65 70 75 80

Ser Val Cys Asp Glu Asp Lys Phe Gly His Asn Glu Phe Ile Gly Glu
85 90 95

Thr Arg Phe Ser Leu Lys Lys Leu Lys Pro Asn Gln Arg Lys Asn Phe
100 105 110

Asn Ile Cys Leu Glu Arg Val Ile Pro Met Lys Arg Ala Gly Thr Thr
115 120 125

Gly Ser Ala Arg
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<210> 18

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 18

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<210> 19
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 19
 gaagatctag gtctatactg ggccac

26

<210> 20
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

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 Gln Thr Arg Val
 20

<210> 21
 <211> 1135
 <212> PRT
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: mammalian
 SYNGAP-C

<400> 21
 Met Gln Ser Phe Lys Glu Ser His Ser His Glu Ser Leu Leu Ser Pro
 1 5 10 15
 Ser Ser Ala Ala Glu Ala Leu Glu Leu Asn Leu Asp Glu Asp Ser Ile
 20 25 30
 Ile Lys Pro Val His Ser Ser Ile Leu Gly Gln Glu Phe Cys Phe Glu
 35 40 45
 Val Thr Thr Ser Ser Gly Thr Lys Cys Phe Ala Cys Arg Ser Ala Ala
 50 55 60
 Glu Arg Asp Lys Trp Ile Glu Asn Leu Gln Arg Ala Val Lys Pro Asn
 65 70 75 80
 Lys Asp Asn Ser Arg Arg Val Asp Asn Val Leu Lys Leu Trp Ile Ile
 85 90 95

Glu	Ala	Arg	Glu	Leu	Pro	Pro	Lys	Lys	Arg	Tyr	Tyr	Cys	Glu	Leu	Cys	100	105	110
Leu	Asp	Asp	Met	Leu	Tyr	Ala	Arg	Thr	Thr	Ser	Lys	Pro	Arg	Ser	Ala	115	120	125
Ser	Gly	Asp	Thr	Val	Phe	Trp	Gly	Glu	His	Phe	Glu	Phe	Asn	Asn	Leu	130	135	140
Pro	Ala	Val	Arg	Ala	Leu	Arg	Leu	His	Leu	Tyr	Arg	Asp	Ser	Asp	Lys	145	150	155
Lys	Arg	Lys	Lys	Asp	Lys	Ala	Gly	Tyr	Val	Gly	Leu	Val	Thr	Val	Pro	165	170	175
Val	Ala	Thr	Leu	Ala	Gly	Arg	His	Phe	Thr	Glu	Gln	Trp	Tyr	Pro	Val	180	185	190
Thr	Leu	Pro	Thr	Gly	Ser	Gly	Gly	Ser	Gly	Gly	Met	Gly	Ser	Gly	Gly	195	200	205
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Lys	Gly	Lys	Gly	Gly	Cys	210	215	220
Pro	Ala	Val	Arg	Leu	Lys	Ala	Arg	Tyr	Gln	Thr	Met	Ser	Ile	Leu	Pro	225	230	235
Met	Glu	Leu	Tyr	Lys	Glu	Phe	Ala	Glu	Tyr	Val	Thr	Asn	His	Tyr	Arg	245	250	255
Met	Leu	Cys	Ala	Val	Leu	Glu	Pro	Ala	Leu	Asn	Val	Lys	Gly	Lys	Glu	260	265	270
Glu	Val	Ala	Ser	Ala	Leu	Val	His	Ile	Leu	Gln	Ser	Thr	Gly	Lys	Ala	275	280	285
Lys	Asp	Phe	Leu	Ser	Asp	Met	Ala	Met	Ser	Glu	Val	Asp	Arg	Phe	Met	290	295	300
Glu	Arg	Glu	His	Leu	Ile	Phe	Arg	Glu	Asn	Thr	Leu	Ala	Thr	Lys	Ala	305	310	315
Ile	Glu	Glu	Tyr	Met	Arg	Leu	Ile	Gly	Gln	Lys	Tyr	Leu	Lys	Asp	Ala	325	330	335
Ile	Gly	Glu	Phe	Ile	Arg	Ala	Leu	Tyr	Glu	Ser	Glu	Glu	Asn	Cys	Glu	340	345	350
Val	Asp	Pro	Ile	Lys	Cys	Thr	Ala	Ser	Ser	Leu	Ala	Glu	His	Gln	Ala	355	360	365
Asn	Leu	Arg	Met	Cys	Cys	Glu	Leu	Ala	Leu	Cys	Lys	Val	Val	Asn	Ser	370	375	380
His	Cys	Val	Phe	Pro	Arg	Glu	Leu	Lys	Glu	Val	Phe	Ala	Ser	Trp	Arg	385	390	395
																		400

Leu Arg Cys Ala Glu Arg Gly Arg Glu Asp Ile Ala Asp Arg Leu Ile
 405 410 415
 Ser Ala Ser Leu Phe Leu Arg Phe Leu Cys Pro Ala Ile Met Ser Pro
 420 425 430
 Ser Leu Phe Gly Leu Met Gln Glu Tyr Pro Asp Glu Gln Thr Ser Arg
 435 440 445
 Thr Leu Thr Leu Ile Ala Lys Val Ile Gln Asn Leu Ala Asn Phe Ser
 450 455 460
 Lys Phe Thr Ser Lys Glu Asp Phe Leu Gly Phe Met Asn Glu Phe Leu
 465 470 475 480
 Glu Leu Glu Trp Gly Ser Met Gln Gln Phe Leu Tyr Glu Ile Ser Asn
 485 490 495
 Leu Asp Thr Leu Thr Asn Ser Ser Ser Phe Glu Gly Tyr Ile Asp Leu
 500 505 510
 Gly Arg Glu Leu Ser Thr Leu His Ala Leu Leu Trp Glu Val Leu Pro
 515 520 525
 Gln Leu Ser Lys Glu Ala Leu Leu Lys Leu Gly Pro Leu Pro Arg Leu
 530 535 540
 Leu Ser Asp Ile Ser Thr Ala Leu Arg Asn Pro Asn Ile Gln Arg Gln
 545 550 555 560
 Pro Ser Arg Gln Ser Glu Arg Ala Arg Ser Gln Pro Met Val Leu Arg
 565 570 575
 Gly Pro Ser Ala Glu Met Gln Gly Tyr Met Met Arg Asp Leu Asn Ser
 580 585 590
 Ser Ile Asp Leu Gln Ser Phe Met Ala Arg Gly Leu Asn Ser Ser Met
 595 600 605
 Asp Met Ala Arg Leu Pro Ser Pro Thr Lys Glu Lys Pro Pro Pro Pro
 610 615 620
 Pro Pro Gly Gly Gly Lys Asp Leu Phe Tyr Val Ser Arg Pro Pro Leu
 625 630 635 640
 Ala Arg Ser Ser Pro Ala Tyr Cys Thr Ser Ser Ser Asp Ile Thr Glu
 645 650 655
 Pro Glu Gln Lys Met Leu Ser Val Asn Lys Ser Val Ser Met Leu Asp
 660 665 670
 Leu Gln Gly Asp Gly Pro Gly Gly Arg Leu Asn Ser Ser Ser Val Ser
 675 680 685
 Asn Leu Ala Ala Val Gly Asp Leu Leu His Ser Ser Gln Ala Ser Leu
 690 695 700

Thr Ala Ala Leu Gly Leu Arg Pro Ala Pro Ala Gly Arg Leu Ser Gln
 705 710 715 720
 Gly Ser Gly Ser Ser Ile Thr Ala Ala Gly Met Arg Leu Ser Gln Met
 725 730 735
 Gly Val Thr Thr Asp Gly Val Pro Ala Gln Gln Leu Arg Ile Pro Leu
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 Ser Phe Gln Asn Pro Leu Phe His Met Ala Ala Asp Gly Pro Gly Pro
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 Pro Ala Gly His Gly Gly Ser Ser Gly His Gly Pro Pro Ser Ser His
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 His His His His His His His His Arg Gly Gly Glu Pro Pro Gly
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 Asp Thr Phe Ala Pro Phe His Gly Tyr Ser Lys Ser Glu Asp Leu Ser
 805 810 815
 Thr Gly Val Pro Lys Pro Pro Ala Ala Ser Ile Leu His Ser His Ser
 820 825 830
 Tyr Ser Asp Glu Phe Gly Pro Ser Gly Thr Asp Phe Thr Arg Arg Gln
 835 840 845
 Leu Ser Leu Gln Asp Asn Leu Gln His Met Leu Ser Pro Pro Gln Ile
 850 855 860
 Thr Ile Gly Pro Gln Arg Pro Ala Pro Ser Gly Pro Gly Gly Gly Ser
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 Gly Gly Gly Ser Gly Gly Gly Gly Gly Gly Gln Pro Pro Pro Leu Gln
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 Arg Gly Lys Ser Gln Gln Leu Thr Val Ser Ala Ala Gln Lys Pro Arg
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 Pro Ser Ser Gly Asn Leu Leu Gln Ser Pro Glu Pro Ser Tyr Gly Pro
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 Ala Ser Glu Arg Thr Val Ala Trp Val Ser Asn Met Pro His Leu Ser
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Glu Tyr Ser Lys Ser Met Asp Glu Ser Arg Leu Asp Arg Val Lys Glu
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 Tyr Glu Glu Glu Ile His Ser Leu Lys Glu Arg Leu His Met Ser Asn
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 Arg Lys Leu Glu Glu Tyr Glu Arg Arg Leu Leu Ser Gln Glu Glu Gln
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 Thr Ser Lys Ile Leu Met Gln Tyr Gln Ala Arg Leu Glu Gln Ser Glu
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 Lys Arg Leu Arg Gln Gln Gln Val Glu Lys Asp Ser Gln Ile Lys Ser
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 Ile Ile Gly Arg Leu Met Leu Val Glu Glu Glu Leu Arg Arg Asp His
 1090 1095 1100
 Pro Ala Met Ala Glu Pro Leu Pro Glu Pro Lys Lys Arg Leu Leu Asp
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<210> 22

<211> 4272

<212> DNA

<213> Unknown Organism

<220>

 <223> Description of Unknown Organism: mammalian
 SYNGAP-A

<400> 22

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<210> 23

<211> 4134

<212> DNA

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: mammalian
SYNGAP-B

<400> 23

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